



SEQUENCE LISTING

<110> John A.
Donovan, Kathleen A.

<120> USE OF GENETICALLY ENGINEERED ANTIBODIES TO CD38 TO TREAT MULTIPLE MYELOMA

<130> 150.188US2

<140> 09/730,374

<141> 2000-12-05

<150> PCT/US99/12512

<151> 1999-06-04

<150> 60/088,277

<151> 1998-08-05

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> A nucleotide sequence encoding a single chain
variable region fragment (scFv)

<400> 1

ggcccagccg gccatggcca aggtccagct gcaggagtca ggacctagcc tagtgcagcc	60
ctcacagcgc ctgtccataa cctgcacagt ctctggtttc tcattaatta gttatggtgt	120
acactggggt cgccagtctc caggaaaggg tctggagtgg ctgggagtga tatggagagg	180
tggaagcaca gactacaatg cagctttcat gtccagactg agcatcacca aggacaactc	240
caagagccaa gttttcttta aaatgaacag tctgcaagct gatgacactg ccatatactt	300
ctgtgccaaa accttgatta cgacgggcta tgctatggac tactggggcc aagggaccac	360
ggtcaccgtc tcctcagggt gaggcgggtc aggcggaggt ggctctggcg gtggcggatc	420
ggacatcgag ctactcagt ctccatcctc cttttctgta tctctaggag acagagtcac	480
cattacttgc aaggcaagtg aggacatata taatcggtta gcctggtatc agcagaaacc	540
aggaatgct cctaggctct taatatctgg tgcaaccagt ttggaaactg gggttccttc	600
aagattcagt ggcaagtggat ctggaaagga ttacactctc agcattacca gtcttcagac	660
tgaagatggt gctacttatt actgtcaaca gtattggagt actcctacgt tcggtggagg	720
gaccaagctg gaaatcaaac gggcggccgc	750

<210> 2

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by an open reading frame of
SEQ ID NO:1

<400> 2

Gly	Pro	Ala	Gly	His	Gly	Gln	Gly	Pro	Ala	Ala	Gly	Val	Arg	Thr	Pro
1				5				10					15		
Ser	Ala	Ala	Leu	Thr	Ala	Pro	Val	His	Asn	Leu	His	Ser	Leu	Trp	Phe
			20					25				30			
Leu	Ile	Asn	Leu	Trp	Cys	Thr	Leu	Gly	Ser	Pro	Val	Ser	Arg	Lys	Gly
			35					40				45			

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Ser Gly Val Ala Gly Ser Asp Met Glu Arg Trp Lys His Arg Leu Gln
 50 55 60
 Cys Ser Phe His Val Gln Thr Glu His His Gln Gly Gln Leu Gln Glu
 65 70 75 80
 Pro Ser Phe Leu Asn Glu Gln Ser Ala Ser His Cys His Ile Leu Leu
 85 90 95
 Cys Gln Asn Leu Asp Tyr Asp Gly Leu Cys Tyr Gly Leu Leu Gly Pro
 100 105 110
 Arg Asp His Gly His Arg Leu Leu Arg Trp Arg Arg Phe Arg Arg Arg
 115 120 125
 Trp Leu Trp Arg Trp Arg Ile Gly His Arg Ala His Ser Val Ser Ile
 130 135 140
 Leu Leu Phe Cys Ile Ser Arg Arg Gln Ser His His Tyr Leu Gln Gly
 145 150 155 160
 Lys Gly His Ile Ser Val Ser Leu Val Ser Ala Glu Thr Arg Lys Cys
 165 170 175
 Ser Ala Leu Asn Ile Trp Cys Asn Gln Phe Gly Asn Trp Gly Ser Phe
 180 185 190
 Lys Ile Gln Trp Gln Trp Ile Trp Lys Gly Leu His Ser Gln His Tyr
 195 200 205
 Gln Ser Ser Asp Arg Cys Cys Tyr Leu Leu Leu Ser Thr Val Leu Glu
 210 215 220
 Tyr Ser Tyr Val Arg Trp Arg Asp Gln Ala Gly Asn Gln Thr Gly Gly
 225 230 235 240
 Arg

<210> 3
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A polypeptide encoded by an open reading frame of
 SEQ ID NO:1

<400> 3
 Ala Gln Pro Ala Met Ala Lys Val Gln Leu Gln Glu Ser Gly Pro Ser
 1 5 10 15
 Leu Val Gln Pro Ser Gln Arg Leu Ser Ile Thr Cys Thr Val Ser Gly
 20 25 30
 Phe Ser Leu Ile Ser Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly
 35 40 45
 Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Arg Gly Gly Ser Thr Asp
 50 55 60
 Tyr Asn Ala Ala Phe Met Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser
 65 70 75 80
 Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asp Asp Thr
 85 90 95
 Ala Ile Tyr Phe Cys Ala Lys Thr Leu Ile Thr Thr Gly Tyr Ala Met
 100 105 110
 Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu
 130 135 140
 Thr Gln Ser Pro Ser Ser Phe Ser Val Ser Leu Gly Asp Arg Val Thr
 145 150 155 160
 Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala Trp Tyr
 165 170 175
 Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu Leu Ile Ser Gly Ala Thr
 180 185 190

Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205
Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr Glu Asp Val Ala
210 215 220
Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Thr Phe Gly Gly Gly
225 230 235 240
Thr Lys Leu Glu Ile Lys Arg Ala Ala
245

<210> 4
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> A polypeptide encoded by an open reading frame of
SEQ ID NO:1

<400> 4
Pro Ser Arg Pro Trp Pro Arg Ser Ser Cys Arg Ser Gln Asp Leu Ala
1 5 10 15
Cys Ser Pro His Ser Ala Cys Pro Pro Ala Gln Ser Leu Val Ser His
20 25 30
Leu Val Met Val Tyr Thr Gly Phe Ala Ser Leu Gln Glu Arg Val Trp
35 40 45
Ser Gly Trp Glu Tyr Gly Glu Val Glu Ala Gln Thr Thr Met Gln Leu
50 55 60
Ser Cys Pro Asp Ala Ser Pro Arg Thr Thr Pro Arg Ala Lys Phe Ser
65 70 75 80
Leu Lys Thr Val Cys Lys Leu Met Thr Leu Pro Tyr Thr Ser Val Pro
85 90 95
Lys Pro Leu Arg Arg Ala Met Leu Trp Thr Thr Gly Ala Lys Gly Pro
100 105 110
Arg Ser Pro Ser Pro Gln Val Glu Ala Val Gln Ala Glu Val Ala Leu
115 120 125
Ala Val Ala Asp Arg Thr Ser Ser Ser Leu Ser Leu His Pro Pro Phe
130 135 140
Leu Tyr Leu Glu Thr Glu Ser Pro Leu Leu Ala Arg Gln Val Arg Thr
145 150 155 160
Tyr Ile Ile Gly Pro Gly Ile Ser Arg Asn Gln Glu Met Leu Leu Gly
165 170 175
Ser Tyr Leu Val Gln Pro Val Trp Lys Leu Gly Phe Leu Gln Asp Ser
180 185 190
Val Ala Val Asp Leu Glu Arg Ile Thr Leu Ser Ala Leu Pro Val Phe
195 200 205
Arg Leu Lys Met Leu Leu Leu Ile Thr Val Asn Ser Ile Gly Val Leu
210 215 220
Leu Arg Ser Val Glu Gly Pro Ser Trp Lys Ser Asn Gly Arg Pro
225 230 235

<210> 5
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> A nucleotide sequence complementary to SEQ ID NO:1
(presented in 5'-3' orientation)

<400> 5
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60

tgttgacagt	aataagtagc	aacatcttca	gtctgaagac	tggtaatgct	gagagtgtaa	120
tcctttccag	atccactgcc	actgaatctt	gaaggaaccc	cagtttccaa	actggttgca	180
ccagatatta	agagcctagg	agcatttcct	ggtttctgct	gataccaggc	taaccgatta	240
tatatgtcct	cacttgccct	gcaagtaatg	gtgactctgt	ctcctagaga	tacagaaaag	300
gaggatggag	actgagttag	ctcgatgtcc	gatccgccac	cgccagagcc	acctccgcct	360
gaaccgcctc	cacctgagga	gacggtgacc	gtgggtccctt	ggccccagta	gtccatagca	420
tagcccgtcg	taatcaagg	tttggcacag	aagtatatgg	cagtgtcatc	agcttgacga	480
ctgttcattt	taaagaaaac	ttggctcttg	gagttgtcct	tggtgatgct	cagtctggac	540
atgaaagctg	cattgtagtc	tgtgcttcca	cctctccata	tcactcccag	ccactccaga	600
ccctttcctg	gagactggcg	aaccagtggt	acaccataac	taattaatga	gaaaccagag	660
actgtgcagg	ttatggacag	gcgctgtgag	ggctgcacta	ggctaggtcc	tgactcctgc	720
agctggacct	tggccatggc	cggctggggc				750